SEQUENCE LISTING

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<110> Goodearl, Andrew
      Glucksmann, Alexandra M.

<120> OCT1P, A PROTEIN HAVING HOMOLOGY TO THE ORGANIC AND SUGAR
      TRANSPORTER FAMILY OF PROTEINS, AND USES THEREOF

<130> 07334/130001

<140> US 09/342,959
<141> 1999-06-29

<150> US 09/107,932
<151> 1998-06-30

<160> 20

<170> FastSEQ for Windows Version 3.0

<210> 1
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<212> DNA
<213> Homo sapiens

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<222> (1)...(2562)
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gctgctccag ggaggaagcg cgcgcgggtgc tgtccagctt cccggtgctg aaaaccggag   120
ggctcgtcat ccaccactac catgtaaggg ccatgagaag ggctcatcct ggcgcagcgc   180
ggac atg gag gag gac tta ttc cag cta agg cag ctg ccg gtt gtg aaa    229
     Met Glu Glu Asp Leu Phe Gln Leu Arg Gln Leu Pro Val Val Lys
      1               5                  10                  15

ttc cgt cgc aca ggc gag agt gca agg tca gag gac gac acg gct tca    277
Phe Arg Arg Thr Gly Glu Ser Ala Arg Ser Glu Asp Asp Thr Ala Ser
              20                  25                  30

gga gag cat gaa gtc cag att gaa ggg gtc cac gtg ggc cta gag gct    325
Gly Glu His Glu Val Gln Ile Glu Gly Val His Val Gly Leu Glu Ala
          35                  40                  45

gtg gag ctg gat gat ggg gca gct gtg ccc aag gag ttt gcc aat ccc    373
Val Glu Leu Asp Asp Gly Ala Ala Val Pro Lys Glu Phe Ala Asn Pro
      50                  55                  60

acc gat gat act ttc atg gtg gaa gat gca gtg gaa gcc att ggc ttt    421
Thr Asp Asp Thr Phe Met Val Glu Asp Ala Val Glu Ala Ile Gly Phe
  65                  70                  75

gga aaa ttt cag tgg aag ctg tct gtt ctc act ggc ttg gct tgg atg    469
Gly Lys Phe Gln Trp Lys Leu Ser Val Leu Thr Gly Leu Ala Trp Met
 80                  85                  90                  95
```

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gct gat gcc atg gag atg atg atc ctc agc atc ctg gca cca cag ctg        517
Ala Asp Ala Met Glu Met Met Ile Leu Ser Ile Leu Ala Pro Gln Leu
                100                 105                 110

cat tgc gag tgg agg ctc cca agc tgg cag gtg gca ttg ctg acc tcg        565
His Cys Glu Trp Arg Leu Pro Ser Trp Gln Val Ala Leu Leu Thr Ser
            115                 120                 125

gtg gtc ttt gta ggc atg atg tcc agc tcc acg ctc tgg gga aat atc        613
Val Val Phe Val Gly Met Met Ser Ser Ser Thr Leu Trp Gly Asn Ile
            130                 135                 140

tca gac cag tac ggc agg aaa aca ggg ctg aag atc agc gtg ctg tgg        661
Ser Asp Gln Tyr Gly Arg Lys Thr Gly Leu Lys Ile Ser Val Leu Trp
        145                 150                 155

act ctg tac tat ggc atc ctt agt gca ttt gcg ccc gtg tat agc tgg        709
Thr Leu Tyr Tyr Gly Ile Leu Ser Ala Phe Ala Pro Val Tyr Ser Trp
160                 165                 170                 175

atc ctg gtg ctc cgg ggc ctg gtg ggc ttc ggg atc gga gga gtt ccc        757
Ile Leu Val Leu Arg Gly Leu Val Gly Phe Gly Ile Gly Gly Val Pro
                180                 185                 190

cag tcg gtg acg ctg tat gcc gag ttc ctt ccc atg aaa gcc aga gct        805
Gln Ser Val Thr Leu Tyr Ala Glu Phe Leu Pro Met Lys Ala Arg Ala
                195                 200                 205

aaa tgt att ttg ctg att gag gta ttc tgg gcc atc ggg aca gtg ttc        853
Lys Cys Ile Leu Leu Ile Glu Val Phe Trp Ala Ile Gly Thr Val Phe
            210                 215                 220

gag gtc gtc ctg gct gtg ttc gtg atg ccc agc ctg ggc tgg cgt tgg        901
Glu Val Val Leu Ala Val Phe Val Met Pro Ser Leu Gly Trp Arg Trp
        225                 230                 235

ctg ctc atc ctc tca gct gtc ccg ctc ctc ctc ttt gcc gtg ctg tgt        949
Leu Leu Ile Leu Ser Ala Val Pro Leu Leu Leu Phe Ala Val Leu Cys
240                 245                 250                 255

ttc tgg ctg cct gaa agt gca agg tat gat gtg ctg tca ggg aac cag        997
Phe Trp Leu Pro Glu Ser Ala Arg Tyr Asp Val Leu Ser Gly Asn Gln
                260                 265                 270

gaa aag gca atc gcc acc tta aag agg ata gca act gaa aac gga gct       1045
Glu Lys Ala Ile Ala Thr Leu Lys Arg Ile Ala Thr Glu Asn Gly Ala
            275                 280                 285

ccc atg ccg ctg ggg aaa ctc atc atc tcc aga cag gaa gac cga ggc       1093
Pro Met Pro Leu Gly Lys Leu Ile Ile Ser Arg Gln Glu Asp Arg Gly
        290                 295                 300

aaa atg agg gac ctt ttc aca ccc cat ttt aga tgg aca act ttg ctg       1141
Lys Met Arg Asp Leu Phe Thr Pro His Phe Arg Trp Thr Thr Leu Leu
        305                 310                 315

ctg tgg ttt ata tgg ttt tcc aat gca ttc tct tac tac ggg tta gtt       1189
Leu Trp Phe Ile Trp Phe Ser Asn Ala Phe Ser Tyr Tyr Gly Leu Val
320                 325                 330                 335
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cta ctc acc aca gaa ctc ttc cag gca gga gat gtc tgc ggc atc tcc    1237
Leu Leu Thr Thr Glu Leu Phe Gln Ala Gly Asp Val Cys Gly Ile Ser
            340             345             350

agt cgg aag aag gct gta gag gca aaa tgc agc ctg gcc tgc gag tac    1285
Ser Arg Lys Lys Ala Val Glu Ala Lys Cys Ser Leu Ala Cys Glu Tyr
            355             360             365

ctg agt gag gag gat tac atg gac ttg ctg tgg acc acc ctc tct gag    1333
Leu Ser Glu Glu Asp Tyr Met Asp Leu Leu Trp Thr Thr Leu Ser Glu
            370             375             380

ttt cca ggt gtc ctt gtg act ctg tgg att att gac cgc ctg ggg cgc    1381
Phe Pro Gly Val Leu Val Thr Leu Trp Ile Ile Asp Arg Leu Gly Arg
            385             390             395

aag aag acc atg gcc ctg tgc ttt gtc atc ttc tcc ttc tgc agc ctc    1429
Lys Lys Thr Met Ala Leu Cys Phe Val Ile Phe Ser Phe Cys Ser Leu
400             405             410             415

ctg ctg ttt atc tgt gtt gga aga aat gtg ctc act ctg tta ctc ttc    1477
Leu Leu Phe Ile Cys Val Gly Arg Asn Val Leu Thr Leu Leu Leu Phe
                420             425             430

att gca aga gcg ttt att tct gga ggc ttt caa gcg gca tat gtt tac    1525
Ile Ala Arg Ala Phe Ile Ser Gly Gly Phe Gln Ala Ala Tyr Val Tyr
            435             440             445

aca cct gag gtc tac ccc acg gca acg cgg gcc ctc ggc ctg ggc acc    1573
Thr Pro Glu Val Tyr Pro Thr Ala Thr Arg Ala Leu Gly Leu Gly Thr
            450             455             460

tgc agc ggc atg gca aga gtg ggt gct ctc atc act ccg ttc atc gcc    1621
Cys Ser Gly Met Ala Arg Val Gly Ala Leu Ile Thr Pro Phe Ile Ala
465             470             475

cag gtg atg ctg gaa tcc tct gtg tac ctg act ctg gca gtt tac agt    1669
Gln Val Met Leu Glu Ser Ser Val Tyr Leu Thr Leu Ala Val Tyr Ser
480             485             490             495

ggc tgc tgc ctc ctg gct gcc ctg gcc tcc tgc ttt ttg ccc att gag    1717
Gly Cys Cys Leu Leu Ala Ala Leu Ala Ser Cys Phe Leu Pro Ile Glu
            500             505             510

acc aaa ggc gga gga ctg cag gag tcc agc cac cgg gag tgg ggc cag    1765
Thr Lys Gly Gly Gly Leu Gln Glu Ser Ser His Arg Glu Trp Gly Gln
            515             520             525

gag atg gtc ggc cga gga atg cac ggt gca ggt gtt acc agg tcg aac    1813
Glu Met Val Gly Arg Gly Met His Gly Ala Gly Val Thr Arg Ser Asn
            530             535             540

tct ggc tct cag gaa tagtgaccga tgggggactg agctggtctt tgaggctgca    1868
Ser Gly Ser Gln Glu
            545

gagcttgggg ggctggcagg ccccaactgg ggcactgatt gtcactgccg acatcaagaa    1928
ctcacccaag agtatgacct ggaccaacag ggttttgtgt cttgactcag tttgctcatc    1988
ttcattgagg tccacccagg gatggggaga tgtttgctct aggggggttct ctgtatatgt    2048
ggtgaaagct ttgttcataa cctgtggatc tacatgggaa gactacccat attaggaggg    2108
tctggtaatg ccagcaacca atcagacacc acccagagtc acccggccaa accctcagtg    2168
aacaaccaaa atatctctct gtagataccg tccaggctca ggcccatgtg acacctgctg    2228
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tccacccacc ggacctgttc agtaggtttc tcccacaccc acagccccag gctttcttct    2288
ttgaaattgc aggcgatcta ggtgtggtct gagcagctat ttcctggcag gggccccccg    2348
gtttgcctcc ctagagcctg accagtggat tctctggcag atggacatgg tgcattcaaa    2408
ctggagccac atgcccccac ccagcccctn ttggagttgc ccgttgttgg caccaagaga    2468
tccagatgtg tcctggggac agctgggtct tgcaccaggt gacaacctca aaacgccgtt    2528
acccccctggg gaactgagga ctgagngcca agtg                                2562
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        <210> 2
        <211> 548
        <212> PRT
        <213> Homo sapiens

        <400> 2
Met Glu Glu Asp Leu Phe Gln Leu Arg Gln Leu Pro Val Val Lys Phe
 1               5                  10                  15
Arg Arg Thr Gly Glu Ser Ala Arg Ser Glu Asp Asp Thr Ala Ser Gly
             20                  25                  30
Glu His Glu Val Gln Ile Glu Gly Val His Val Gly Leu Glu Ala Val
         35                  40                  45
Glu Leu Asp Asp Gly Ala Ala Val Pro Lys Glu Phe Ala Asn Pro Thr
     50                  55                  60
Asp Asp Thr Phe Met Val Glu Asp Ala Val Glu Ala Ile Gly Phe Gly
 65              70                  75                  80
Lys Phe Gln Trp Lys Leu Ser Val Leu Thr Gly Leu Ala Trp Met Ala
             85                  90                  95
Asp Ala Met Glu Met Met Ile Leu Ser Ile Leu Ala Pro Gln Leu His
            100                 105                 110
Cys Glu Trp Arg Leu Pro Ser Trp Gln Val Ala Leu Leu Thr Ser Val
            115                 120                 125
Val Phe Val Gly Met Met Ser Ser Ser Thr Leu Trp Gly Asn Ile Ser
        130                 135                 140
Asp Gln Tyr Gly Arg Lys Thr Gly Leu Lys Ile Ser Val Leu Trp Thr
145                 150                 155                 160
Leu Tyr Tyr Gly Ile Leu Ser Ala Phe Ala Pro Val Tyr Ser Trp Ile
                165                 170                 175
Leu Val Leu Arg Gly Leu Val Gly Phe Gly Ile Gly Gly Val Pro Gln
            180                 185                 190
Ser Val Thr Leu Tyr Ala Glu Phe Leu Pro Met Lys Ala Arg Ala Lys
            195                 200                 205
Cys Ile Leu Leu Ile Glu Val Phe Trp Ala Ile Gly Thr Val Phe Glu
        210                 215                 220
Val Val Leu Ala Val Phe Val Met Pro Ser Leu Gly Trp Arg Trp Leu
225                 230                 235                 240
Leu Ile Leu Ser Ala Val Pro Leu Leu Leu Phe Ala Val Leu Cys Phe
                245                 250                 255
Trp Leu Pro Glu Ser Ala Arg Tyr Asp Val Leu Ser Gly Asn Gln Glu
            260                 265                 270
Lys Ala Ile Ala Thr Leu Lys Arg Ile Ala Thr Glu Asn Gly Ala Pro
            275                 280                 285
Met Pro Leu Gly Lys Leu Ile Ile Ser Arg Gln Glu Asp Arg Gly Lys
        290                 295                 300
Met Arg Asp Leu Phe Thr Pro His Phe Arg Trp Thr Thr Leu Leu Leu
305                 310                 315                 320
Trp Phe Ile Trp Phe Ser Asn Ala Phe Ser Tyr Tyr Gly Leu Val Leu
                325                 330                 335
Leu Thr Thr Glu Leu Phe Gln Ala Gly Asp Val Cys Gly Ile Ser Ser
            340                 345                 350
Arg Lys Lys Ala Val Glu Ala Lys Cys Ser Leu Ala Cys Glu Tyr Leu
            355                 360                 365
Ser Glu Glu Asp Tyr Met Asp Leu Leu Trp Thr Thr Leu Ser Glu Phe
        370                 375                 380
```

```
Pro Gly Val Leu Val Thr Leu Trp Ile Ile Asp Arg Leu Gly Arg Lys
385             390             395             400
Lys Thr Met Ala Leu Cys Phe Val Ile Phe Ser Phe Cys Ser Leu Leu
                405             410             415
Leu Phe Ile Cys Val Gly Arg Asn Val Leu Thr Leu Leu Leu Phe Ile
            420             425             430
Ala Arg Ala Phe Ile Ser Gly Gly Phe Gln Ala Ala Tyr Val Tyr Thr
        435             440             445
Pro Glu Val Tyr Pro Thr Ala Thr Arg Ala Leu Gly Leu Gly Thr Cys
    450             455             460
Ser Gly Met Ala Arg Val Gly Ala Leu Ile Thr Pro Phe Ile Ala Gln
465             470             475             480
Val Met Leu Glu Ser Ser Val Tyr Leu Thr Leu Ala Val Tyr Ser Gly
                485             490             495
Cys Cys Leu Leu Ala Ala Leu Ala Ser Cys Phe Leu Pro Ile Glu Thr
            500             505             510
Lys Gly Gly Gly Leu Gln Glu Ser Ser His Arg Glu Trp Gly Gln Glu
        515             520             525
Met Val Gly Arg Gly Met His Gly Ala Gly Val Thr Arg Ser Asn Ser
    530             535             540
Gly Ser Gln Glu
545
```

        <210> 3
        <211> 1644
        <212> DNA
        <213> Homo sapiens

        <400> 3

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atggaggagg acttattcca gctaaggcag ctgccggttg tgaaattccg tcgcacaggc    60
gagagtgcaa ggtcagagga cgacacggct tcaggagagc atgaagtcca gattgaaggg   120
gtccacgtgg gcctagaggc tgtggagctg gatgatgggg cagctgtgcc caaggagttt   180
gccaatccca ccgatgatac tttcatggtg gaagatgcag tggaagccat tggctttgga   240
aaatttcagt ggaagctgtc tgttctcact ggcttggctt ggatggctga tgccatggag   300
atgatgatcc tcagcatcct ggcaccacag ctgcattgcg agtggaggct cccaagctgg   360
caggtggcat tgctgacctc ggtggtcttt gtaggcatga tgtccagctc cacgctctgg   420
ggaaatatct cagaccagta cggcaggaaa acagggctga agatcagcgt gctgtggact   480
ctgtactatg gcatccttag tgcatttgcg cccgtgtata gctggatcct ggtgctccgg   540
ggcctggtgg gcttcgggat cggaggagtt ccccagtcgg tgacgctgta tgccgagttc   600
cttcccatga agccagagc taaatgtatt ttgctgattg aggtattctg gccatcggg    660
acagtgttcg aggtcgtcct ggctgtgttc gtgatgccca gcctgggctg gcgttggctg   720
ctcatcctct cagctgtccc gctcctcctc tttgccgtgc tgtgtttctg gctgcctgaa   780
agtgcaaggt atgatgtgct gtcaggaac caggaaaag caatcgccac cttaaagagg   840
atagcaactg aaaacggagc tcccatgccg ctggggaaac tcatcatctc cagacaggaa   900
gaccgaggca aatgaggga cctttcaca ccccatttta gatggacaac tttgctgctg   960
tggtttatat ggttttccaa tgcattctct tactacgggt tagttctact caccacagaa  1020
ctcttccagg caggagatgt ctgcggcatc tccagtcgga agaaggctgt agaggcaaaa  1080
tgcagcctgg cctgcgagta cctgagtgag gaggattaca tggacttgct gtggaccacc  1140
ctctctgagt ttccaggtgt ccttgtgact ctgtggatta ttgaccgcct ggggcgcaag  1200
aagaccatgg ccctgtgctt tgtcatcttc tccttctgca gcctcctgct gtttatctgt  1260
gttggaagaa atgtgctcac tctgttactc ttcattgcaa gagcgtttat ttctggaggc  1320
tttcaagcgg catatgttta cacacctgag gtctacccca cggcaacgcg ggcctcggc   1380
ctgggcacct gcagcggcat ggcaagagtg ggtgctctca tcactccgtt catcgcccag  1440
gtgatgctgg aatcctctgt gtacctgact ctggcagttt acagtggctg ctgcctcctg  1500
gctgccctgg cctcctgctt tttgcccatt gagaccaaag cggaggact gcaggagtcc  1560
agccaccggg agtggggcca ggagatggtc ggccgaggaa tgcacggtgc aggtgttacc  1620
aggtcgaact ctggctctca ggaa                                         1644
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        <210> 4
        <211> 273
        <212> PRT
        <213> Homo sapiens

<400> 4

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Glu Asp Ala Val Glu Ala Ile Gly Phe Gly Lys Phe Gln Trp Lys Leu
1               5                   10                  15
Ser Val Leu Thr Gly Leu Ala Trp Met Ala Asp Ala Met Glu Met Met
            20                  25                  30
Ile Leu Ser Ile Leu Ala Pro Gln Leu His Cys Glu Trp Arg Leu Pro
        35                  40                  45
Ser Trp Gln Val Ala Leu Leu Thr Ser Val Val Phe Val Gly Met Met
    50                  55                  60
Ser Ser Ser Thr Leu Trp Gly Asn Ile Ser Asp Gln Tyr Gly Arg Lys
65                  70                  75                  80
Thr Gly Leu Lys Ile Ser Val Leu Trp Thr Leu Tyr Tyr Gly Ile Leu
            85                  90                  95
Ser Ala Phe Ala Pro Val Tyr Ser Trp Ile Leu Val Leu Arg Gly Leu
        100                 105                 110
Val Gly Phe Gly Ile Gly Gly Val Pro Gln Ser Val Thr Leu Tyr Ala
        115                 120                 125
Glu Phe Leu Pro Met Lys Ala Arg Ala Lys Cys Ile Leu Leu Ile Glu
    130                 135                 140
Val Phe Trp Ala Ile Gly Thr Val Phe Glu Val Val Leu Ala Val Phe
145                 150                 155                 160
Val Met Pro Ser Leu Gly Trp Arg Trp Leu Leu Ile Leu Ser Ala Val
            165                 170                 175
Pro Leu Leu Leu Phe Ala Val Leu Cys Phe Trp Leu Pro Glu Ser Ala
            180                 185                 190
Arg Tyr Asp Val Leu Ser Gly Asn Gln Glu Lys Ala Ile Ala Thr Leu
    195                 200                 205
Lys Arg Ile Ala Thr Glu Asn Gly Ala Pro Met Pro Leu Gly Lys Leu
    210                 215                 220
Ile Ile Ser Arg Gln Glu Asp Arg Gly Lys Met Arg Asp Leu Phe Thr
225                 230                 235                 240
Pro His Phe Arg Trp Thr Thr Leu Leu Leu Trp Phe Ile Trp Phe Ser
            245                 250                 255
Asn Ala Phe Ser Tyr Tyr Gly Leu Val Leu Leu Thr Thr Glu Leu Phe
            260                 265                 270
Gln
```

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<210> 5
<211> 293
<212> PRT
<213> Homo sapiens
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<400> 5

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Trp Cys Phe Met Ala Ala Phe Gly Gly Met Phe Met Phe Gly Trp Asp
1               5                   10                  15
Thr Gly Val Ile Asn Gly Phe Val Trp Met Ile Asp Phe His Tyr Arg
            20                  25                  30
Phe Gly Met Met His Tyr Asp Trp Thr Tyr Tyr Leu Ser Thr Met Arg
        35                  40                  45
Trp Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Met Ile Gly Ser
    50                  55                  60
Ile Phe Phe Gly Trp Ile Gly Asp Met Tyr Gly Arg Arg Met Ser Met
65                  70                  75                  80
Met Met Val Asn Val Ile Phe Ile Ile Gly Ile Ile Ile Met Ile Phe
            85                  90                  95
Ser Ile Asn Tyr Ser Trp Trp Met Tyr Ile Ile Gly Arg Ile Ile Met
        100                 105                 110
Gly Ile Gly Val Gly Gly Ile Ser Val Leu Val Pro Met Tyr Ile Ser
        115                 120                 125
Glu Ile Ala Pro Lys His Leu Arg Gly Thr Met Val Ser Trp Tyr Gln
    130                 135                 140
```

```
Leu Met Ile Thr Ile Gly Ile Phe Ile Ala Tyr Cys Phe Asn Tyr Gly
145             150             155             160
Phe Asn Tyr Tyr Asn Asn Asp Ser Trp Gln Trp Arg Trp Pro Leu Gly
            165             170             175
Leu Cys Phe Ile Trp Ala Ile Phe Met Ile Ile Gly Met Met Phe Leu
            180             185             190
Pro Glu Ser Pro Arg Trp Leu Val Ile Lys Gly Arg Ile Glu Glu Ala
            195             200             205
Arg Arg Ser Leu Gln Arg Leu Arg Gly Trp Asp Asp Val Asp Pro Glu
            210             215             220
Ile Gln Glu Met Met Asp Glu Ile Glu Ala Met Ile Glu Glu Glu Leu
225             230             235             240
Ala Gly Asn Ala Ser Trp Gly Glu Leu Phe Arg Arg Arg Thr Pro Lys
            245             250             255
Met Arg Trp Arg Ile Ile Met Gly Met Met Ile Gln Ile Phe Gln Gln
            260             265             270
Phe Thr Gly Ile Asn Tyr Ile Met Tyr Tyr Ser Thr Thr Ile Phe Glu
            275             280             285
Ser Val Gly Met Gln
            290


        <210> 6
        <211> 23
        <212> PRT
        <213> Homo sapiens


        <400> 6
Leu Ser Val Leu Thr Gly Leu Ala Trp Met Ala Asp Ala Met Glu Met
  1             5               10              15
Met Ile Leu Ser Ile Leu Ala
            20


        <210> 7
        <211> 19
        <212> PRT
        <213> Homo sapiens


        <400> 7
Val Ala Leu Leu Thr Ser Val Val Phe Val Gly Met Met Ser Ser Ser
  1             5               10              15
Thr Leu Trp


        <210> 8
        <211> 21
        <212> PRT
        <213> Homo sapiens


        <400> 8
Ile Ser Val Leu Trp Thr Leu Tyr Tyr Gly Ile Leu Ser Ala Phe Ala
  1             5               10              15
Pro Val Tyr Ser Trp
            20


        <210> 9
        <211> 17
        <212> PRT
        <213> Homo sapiens


        <400> 9
Leu Val Gly Phe Gly Ile Gly Gly Val Pro Gln Ser Val Thr Leu Tyr
  1             5               10              15
```

Ala

        <210> 10
        <211> 24
        <212> PRT
        <213> Homo sapiens

        <400> 10
Cys Ile Leu Leu Ile Glu Val Phe Trp Ala Ile Gly Thr Val Phe Glu
 1   5   10   15
Val Val Leu Ala Val Phe Val Met
            20

        <210> 11
        <211> 20
        <212> PRT
        <213> Homo sapiens

        <400> 11
Trp Leu Leu Ile Leu Ser Ala Val Pro Leu Leu Leu Phe Ala Val Leu
 1   5   10   15
Cys Phe Trp Leu
            20

        <210> 12
        <211> 23
        <212> PRT
        <213> Homo sapiens

        <400> 12
Trp Thr Thr Leu Leu Leu Trp Phe Ile Trp Phe Ser Asn Ala Phe Ser
 1   5   10   15
Tyr Tyr Gly Leu Val Leu Leu
            20

        <210> 13
        <211> 19
        <212> PRT
        <213> Homo sapiens

        <400> 13
Leu Leu Trp Thr Thr Leu Ser Glu Phe Pro Gly Val Leu Val Thr Leu
 1   5   10   15
Trp Ile Ile

        <210> 14
        <211> 19
        <212> PRT
        <213> Homo sapiens

        <400> 14
Met Ala Leu Cys Phe Val Ile Phe Ser Phe Cys Ser Leu Leu Leu Phe
 1   5   10   15
Ile Cys Val

        <210> 15
        <211> 20
        <212> PRT
        <213> Homo sapiens

        <400> 15
Leu Leu Leu Phe Ile Ala Arg Ala Phe Ile Ser Gly Gly Phe Gln Ala
 1   5   10   15
Ala Tyr Val Tyr
            20

        <210> 16
        <211> 22
        <212> PRT
        <213> Homo sapiens

        <400> 16
Ala Leu Gly Leu Gly Thr Cys Ser Gly Met Ala Arg Val Gly Ala Leu
 1   5   10   15
Ile Thr Pro Phe Ile Ala
            20

        <210> 17
        <211> 24
        <212> PRT
        <213> Homo sapiens

        <400> 17
Val Tyr Leu Thr Leu Ala Val Tyr Ser Gly Cys Cys Leu Leu Ala Ala
 1   5   10   15
Leu Ala Ser Cys Phe Leu Pro Ile
            20

        <210> 18
        <211> 24
        <212> DNA
        <213> Homo sapiens

        <400> 18
tccatgtccg cgctgcgcca ggat   24

        <210> 19
        <211> 19
        <212> DNA
        <213> Homo sapiens

        <400> 19
ttagctggaa taagtcctc   19

        <210> 20
        <211> 1906
        <212> DNA
        <213> Rattus rattus

        <400> 20
gtcgacccac gcgtccgagc aaagaggatt acatggacct gctgtggacc accctgtctg   60
agttcccagg tgtccttgtg actctgtggg tcatcgaccg cctgggccgc aagaagacca   120
tggctctgtg tttcgtcatc ttttccctct gcagcctcct gctgttcatc tgcattggaa   180
gaaatgtgct aaccctctta ctgttcattg caagagcgtt tatttctgga ggcttccaag   240
cagcctacgt ttacacgcct gaggtgtatc caacggcgac gagggcgctg ggcctgggca   300
cctgcagcgg catggcgaga gtgggcgcgc tcatcactcc attcatagct caggtgatgc   360
tggaatcttc cgtgtacctg accctggccg tctacagtgg ctgctgcctc cttgctgcct   420
tggcctcctg ctttctgccc atcgagacca aaggccgagc actgcaggag tccagccacc   480
gggagtgggg ccaggagatg gttggccgag ggacaaacag cacaggcgtc cccaggtcga   540
actctggctc tcaggagtag tgacccctgg gagttgagct ggtctttgag gccggagcct   600
agaaagctgg cagagcccag ctgggccact aacggtcact gccgacatca gaactttcc   660
ccgagtgggc gaagtgaacc gacagggttt tgtgtcttca ctgtgtttgg cctatgttca   720

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